

**ABSTRACT**

5 A method of determining the presence and identity of a variation in a nucleotide sequence between a first polynucleotide and a second polynucleotide, comprising a) providing a sample of the first polynucleotide; b) selecting a region of the first polynucleotide potentially containing the variation; c) subjecting the selected region to a template producing amplification reaction to produce a first plurality of double stranded polynucleotide templates which include the selected region; d) selecting a region of the first polynucleotide sequence lying within the templates for analysis; e) producing a family of labeled, linear polynucleotide fragments from both strands of the templates simultaneously by a fragment producing reaction.